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RAW SEQUENCE LISTING
PATENT APPLICATION US/08/753,750

DATE: 09/04/97
TIME: 14:55:06

1817

INPUT SET: S20107.raw

> This Raw Listing contains the General
> Information Section and up to the first 5 pages.

```
 1                               SEQUENCE LISTING        ENTERED
 2
 3    (1)     General Information:
 4
 5        (i)  APPLICANT: Lo, Reggie Y.C.
 6                        Schryvers, Anthony B.
 7                        Potter, Andrew A
 8
 9       (ii)  TITLE OF INVENTION: Transferrin Binding Proteins of
10             Pasteurella Haemolytica and Vaccines Containing Same
11
12      (iii)  NUMBER OF SEQUENCES: 52
13
14       (iv)  CORRESPONDENCE ADDRESS:
15             (A)  ADDRESSEE: BAKER & BOTTS
16             (B)  STREET: 1299 Pennsylvania Avenue
17             (C)  CITY: Washington
18             (D)  STATE: D.C.
19             (E)  COUNTRY: U.S.A.
20             (F)  ZIP: 20004-2400
21
22        (v)  COMPUTER READABLE FORM:
23             (A)  MEDIUM TYPE: Floppy disk
24             (B)  COMPUTER: IBM PC compatible
25             (C)  OPERATING SYSTEM: PC-DOS/MS-DOS
26             (D)  SOFTWARE: PatentIn Release #1.0, Version #1.30
27
28       (vi)  CURRENT APPLICATION DATA:
29             (A)  APPLICATION NUMBER: US 08/753,750
30             (B)  FILING DATE: 29-NOV-1996
31             (C)  CLASSIFICATION:
32
33      (vii)  PRIOR APPLICATION DATA:
34             (A)  APPLICATION NUMBER: US 60/008,569
35             (B)  FILING DATE: 01-DEC-1995
36
37      (vii)  PRIOR APPLICATION DATA:
38             (A)  APPLICATION NUMBER: CA 2,164,274
39             (B)  FILING DATE: 01-DEC-1995
40
41     (viii)  ATTORNEY/AGENT INFORMATION:
42             (A)  NAME: Remenick, James
43             (B)  REGISTRATION NUMBER: 36,902
44             (C)  REFERENCE/DOCKET NUMBER: 63637-0102
45
46       (ix)  TELECOMMUNICATION INFORMATION:
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RAW SEQUENCE LISTING
PATENT APPLICATION *US/08/753,750*

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TIME: 14:55:08

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47              (A) TELEPHONE: (202) 639-7996
48              (B) TELEFAX: (202) 639-7890
49
50
51   (2) INFORMATION FOR SEQ ID NO:1:
52
53        (i) SEQUENCE CHARACTERISTICS:
54              (A) LENGTH: 2784 base pairs
55              (B) TYPE: nucleic acid
56              (C) STRANDEDNESS: single
57              (D) TOPOLOGY: linear
58
59       (ii) MOLECULE TYPE: DNA (genomic)
60
61       (vi) ORIGINAL SOURCE:
62              (A) ORGANISM: Pasteurella haemolytica (tbpA gene)
63              (B) STRAIN: H196
64
65
66
67       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
68
69   ATGATAATGA AATATCATCA TTTTCGCTAT TCACCTGTTG CCTTAACAGT GTTATTTGCT        60
70
71   CTTTCTCATT CATACGGTGC TGCGACTGAA AATAAAAAAA TCGAAGAAAA TAACGATCTA       120
72
73   GCTGTTCTGG ATGAAGTTAT TGTGACAGAG AGCCATTATG CTCACGAACG TCAAAACGAA       180
74
75   GTAACTGGCT TGGGGAAAGT AGTGAAAAAT TATCACGAAA TGAGTAAAAA TCAAATTCTT       240
76
77   GGTATTCGTG ATTTAACTCG CTATGACCCT GGTATTTCGG TGGTGGAACA AGGTCGCGGT       300
78
79   GCAAGTAGTG GCTATGCCAT TCGAGGTGTA GATAAAAACC GTGTCAGCTT ACTTGTTGAT       360
80
81   GGGCTACCAC AAGCGCACAG TTATCATACG CTAGGTTCAG ATGCTAATGG TGGTGCAATT       420
82
83   AATGAGATTG AGTATGAAAA CATTCGTTCA ·ATTGAGTTAA GCAAAGGAGC AAGTTCTGCG       480
84
85   GAATATGGCT CTGGTGCGCA TGGTGGTGCT ATTGGTTTTC GTACTAAAGA TGCGCAGGAT       540
86
87   ATTATTAAAG AGGGGCAGCA TTGGGGCTTA GATAGTAAGA CCTCTTATGC CAGCAAAAAT       600
88
89   AGCCATTTTT TACAGTCTAT CGCAGCGGCT GGTGAGGCGG GTGGTTTTGA AGCACTTGTT       660
90
91   ATTGCAACTC ACCGACACGG TAAAGAGACC AAAATTCATT CCGAGGCAAA TAAATTAAAA       720
92
93   CATAATATTC GGCGTATAAC CGGCTﻬTGAA AATCGCTACG ACTTTACCCA AATTCCGCAC       780
94
95   AGAATGCTCC TGGAGGATCT ﻬCTTTTAATT GTGGAAGATA CTTGCCCAAC ATTAGATTGT       840
96
97   ACTCCTCGTG CAAGGGTTAA ﻬTTGAACCGC GATAATTTCC CAGTGAGAAC ATTTCCGGAA       900
98
99   TATACGCCTG AAGAGCGCAA ACAGCTTGAG CAGATTCCTT ATCGCACTGA GCAGCTCTCA       960
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RAW SEQUENCE LISTING
PATENT APPLICATION   US/08/753,750

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TIME: 14:55:10

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101    GCCCAAGAAT ATACCGGTAA AGATCGCATT GCACCAAACC CTTTAGATTA CAAGAGTAAT    1020
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103    TCTGTTTTTA TGAAGTTTGG CTATCACTTC AACTCGTCTC ATTATCTTGG CGCAATCTTA    1080
104
105    GAAGATACAA AAACACGCTA CGATATCCGT GATATGCAAA CGCCAGCTTA CTATACAAAA    1140
106
107    GACGATATTA ACTTATCACT TAGGAACTAT GTTTATGAAG GGGATAATAT TTTAGATGGC    1200
108
109    TTAGTGTTCA AGCCAAGGAT CCCTTATGGG TTGCGCTATA GCCATGTGAA GTTTTTTGAT    1260
110
111    GAACGTCACC ACAAACGTCG TTTAGGATTC ACCTATAAAT ATAAACCAGA GAATAATCGC    1320
112
113    TGGTTGGATA GCATTAAACT CAGTGCGGAT AAACAAGATA TTGAACTATA TAGCCGGCTA    1380
114
115    CATCGCTTGC ATTGTAGCGA TTATCCTGTG GTAGATAAAA ATTGCCGCCC GACTTTGGAT    1440
116
117    AAATCTTGGT CTATGTATCG AACTGAGCGT AATAATTACC AAGAAAAGCA TCGTGTCATT    1500
118
119    CATTTAGAAT TTGATAAAGC GCTAAATGCT GGTCAAGGCG TATTTAACCA AACCCACAAA    1560
120
121    CTGAATTTAG GGTTGGGCTT TGATCGATTT AATTCGCTTA TGGATCATGG GGATATGACT    1620
122
123    GCCCAATATA CCAAAGGCGG TTATACCAGC TACCGCGGTA GAGGGCGTTT AGATAATCCA    1680
124
125    TATATTTATC GCCGCGATCC ACGCAGTATT GAAACGGTAT CTTTGTGTAA TAATACACGC    1740
126
127    GGCGACATCT TAAACTGTGA ACCGCGTAAA ATTAAAGGCG ATAGCCATTT TGTTAGCTTC    1800
128
129    CGCGATCTAG TGATAAGCGA GTATGTGGAT TTGGGATTAG GGGTGCGTTT TGATCAACAT    1860
130
131    CGATTTAAAT CTGATGATCC GTGGACACTT AGCCGAACTT ATCGAAATTG GTCTTGGAAT    1920
132
133    GGTGGGATTA CGCTTAAACC AACAGAGTTT GTATCGCTTT CTTATCGCAT TTCAAACGGT    1980
134
135    TTTAGAGTGC CTGCATTCTA TGAACTTTAT GGTAAACGTG ATCATATTGG GCTTAAAGAT    2040
136
137    AACGAATATG TGCAACGCGC GCAACGTAGC CACCAGTTAG AGCCAGAAAA ATCGACTAAT    2100
138
139    CATGAGATTG GAGTTAGCTT TAAAGGTCAA TTTGGTTACC TTGAATTTCC GTAATAACTA    2160
140
141    TAAAAATATG ATTGCGACAG CATGTAAAAG AATAATACAA AAATCACACT GTTTCTATAA    2220
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143    CTACCATAAT ATTCAAGATG TAGCACTAAA CGGGATAAAT TTAGTCGCTA AATTTGACTT    2280
144
145    ACACGGTATT TTATCTATGC TGCCAGATGG TTTTTATTCA TCAGTTGCTT ATAACCGTGT    2340
146
147    AAAAGTAAAA GAGCGGAAAC TAACCGACTC AAGACTCGAT AGCGTAAACG ATCCTATTCT    2400
148
149    AGATGCGATT CAGCCAGCAC GCTATGTGCT TGGATTCGGC TACGATCACC CAGAAGAAAA    2460
150
151    ATGGGGAATT GGCATTACTA CCACCTATTC TAAAGCCAAA AACGCCGATG AGGTGGCAGG    2520
152
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153   CACACGTCAT CACGGATACA TCGCGTTGAT TTAGGTGGCA AACTGACCGG TTCTTGGTAC   2580
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155   ACCCATGATA TTACCGGTTA CATCAATTAT AAAAACTACA CCTTACGTGG AGGAATTTAT   2640
156
157   AATGTGACTA ATCGTAAATA TTCCACTTGG GAATCAGTGC GCCAATCCGG TGTGAATGCA   2700
158
159   GTAAACCAAG ACCGGGGTAG CAATTACACT CGATTTGGCG CTCCGGGGAG AAATTTCAGT   2760
160
161   TTAGCATTTG AAATGAAGTT TTAG                                          2784
162
163   (2) INFORMATION FOR SEQ ID NO:2:
164
165        (i) SEQUENCE CHARACTERISTICS:
166             (A) LENGTH: 930 amino acids
167             (B) TYPE: amino acid
168             (C) STRANDEDNESS: single
169             (D) TOPOLOGY: linear
170
171       (ii) MOLECULE TYPE: protein
172
173       (vi) ORIGINAL SOURCE:
174             (A) ORGANISM: Pasteurella haemolytica (TbpA protein)
175
176
177
178       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
179
180       Met Ile Met Lys Tyr His His Phe Arg Tyr Ser Pro Val Ala Leu Thr
181       1               5                   10                  15
182
183       Val Leu Phe Ala Leu Ser His Ser Tyr Gly Ala Ala Thr Glu Asn Lys
184                   20                  25                  30
185
186       Lys Ile Glu Glu Asn Asn Asp Leu Ala Val Leu Asp Glu Val Ile Val
187                   35                  40                  45
188
189       Thr Glu Ser His Tyr Ala His Glu Arg Gln Asn Glu Val Thr Gly Leu
190           50                  55                  60
191
192       Gly Lys Val Val Lys Asn Tyr His Glu Met Ser Lys Asn Gln Ile Leu
193       65                  70                  75                  80
194
195       Gly Ile Arg Asp Leu Thr Arg Tyr Asp Pro Gly Ile Ser Val Val Glu
196                   85                  90                  95
197
198       Gln Gly Arg Gly Ala Ser Ser Gly Tyr Ala Ile Arg Gly Val Asp Lys
199                   100               105                 110
200
201       Asn Arg Val Ser Leu Leu Val Asp Gly Leu Pro Gln Ala His Ser Tyr
202                   115                 120                 125
203
204       His Thr Leu Gly Ser Asp Ala Asn Gly Gly Ala Ile Asn Glu Ile Glu
205           130                 135                 140
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206
207     Tyr Glu Asn Ile Arg Ser Ile Glu Leu Ser Lys Gly Ala Ser Ser Ala
208     145             150                 155                 160
209
210     Glu Tyr Gly Ser Gly Ala His Gly Gly Ala Ile Gly Phe Arg Thr Lys
211                     165             170                 175
212
213     Asp Ala Gln Asp Ile Ile Lys Glu Gly Gln His Trp Gly Leu Asp Ser
214                 180             185                 190
215
216     Lys Thr Ser Tyr Ala Ser Lys Asn Ser His Phe Leu Gln Ser Ile Ala
217             195             200                 205
218
219     Ala Ala Gly Glu Ala Gly Gly Phe Glu Ala Leu Val Ile Ala Thr His
220         210                 215                 220
221
222     Arg His Gly Lys Glu Thr Lys Ile His Ser Glu Ala Asn Lys Leu Lys
223     225                 230                 235                 240
224
225     His Asn Ile Arg Arg Ile Thr Gly Phe Glu Asn Arg Tyr Asp Phe Thr
226                     245                 250                 255
227
228     Gln Ile Pro His Arg Met Leu Leu Glu Asp Leu Leu Leu Ile Val Glu
229                 260                 265                 270
230
231     Asp Thr Cys Pro Thr Leu Asp Cys Thr Pro Arg Ala Arg Val Lys Leu
232             275                 280                 285
233
234     Asn Arg Asp Asn Phe Pro Val Arg Thr Phe Pro Glu Tyr Thr Pro Glu
235         290                 295                 300
236
237     Glu Arg Lys Gln Leu Glu Gln Ile Pro Tyr Arg Thr Glu Gln Leu Ser
238     305                 310                 315                 320
239
240     Ala Gln Glu Tyr Thr Gly Lys Asp Arg Ile Ala Pro Asn Pro Leu Asp
241                     325                 330                 335
242
243     Tyr Lys Ser Asn Ser Val Phe Met Lys Phe Gly Tyr His Phe Asn Ser
244             340                 345                 350
245
246     Ser His Tyr Leu Gly Ala Ile Leu Glu Asp Thr Lys Thr Arg Tyr Asp
247             355                 360                 365
248
249     Ile Arg Asp Met Gln Thr Pro Ala Tyr Tyr Thr Lys Asp Asp Ile Asn
250         370                 375                 380
251
252  ∘  Leu Ser Leu Arg Asn Tyr Val Tyr Glu Gly Asp Asn Ile Leu Asp Gly
253     385                 390                 395                 400
254
255     Leu Val Phe Lys Pro Arg Ile Pro Tyr Gly Leu Arg Tyr Ser His Val
256                     405                 410                 415
257
258     Lys Phe Phe Asp Glu Arg His His Lys Arg Arg Leu Gly Phe Thr Tyr
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SEQUENCE VERIFICATION REPORT
PATENT APPLICATION *US/08/753,750*

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